

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2000, 10:23:53 ; Search time 8511.27 Seconds
(without alignments)
348.684 Million cell updates/sec

Title: US-09-270-910-36

Perfect score: 480

Sequence: 1 ggigtgttaattatgagac.....actcagatgcctaacactaa 480

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
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29: gb_est29:*
30: gb_est30:*
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35: gb_est35:*
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37: gb_est37:*
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39: gb_est39:*
40: gb_est40:*
41: em_estba:*
42: em_estfun:*
43: em_esthum1:*

44: em_esthum2:*
45: em_esthum3:*
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47: em_esthum5:*
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56: em_esthum14:*
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58: em_esthum16:*
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76: em_estrov2:*
77: em_estrov3:*
78: em_estrov4:*
79: em_estrov5:*
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82: em_estrov8:*
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84: em_estrov10:*
85: em_estrov11:*
86: em_estrov12:*
87: em_estrov13:*
88: gb_gss1:*
89: gb_gss2:*
90: gb_gss3:*
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93: em_gss2:*
94: em_gss3:*
95: em_gss4:*
96: gb_gss5:*
97: gb_gss6:*
98: gb_gss7:*
99: gb_gss8:*
100: gb_gss9:*
101: em_gss5:*
102: em_gss6:*
103: em_gss7:*
104: em_gss8:*
105: em_gss9:*
106: em_gss10:*
107: em_gss11:*
108: gb_gss10:*
109: gb_gss11:*
110: em_gss12:*
111: gb_gss12:*
112: gb_gss13:*
113: gb_gss14:*
114: gb_gss15:*
115: gb_gss16:*
116: gb_gss17:*

117: qb_gss18: *
118: qb_gss19: *
119: em_gss13: *
120: qb_gss20: *
121: qb_gss21: *
122: qb_gss22: *
123: qb_gss23: *
124: qb_gss24: *
125: em_gss14: *
126: em_gss15: *
127: em_gss16: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	180	37.5	551	24	AM719509 LjNEST5d9
2	171	35.6	536	24	AM782077 sm01b05.y
3	166.6	34.7	698	25	AM980848 EST392001
4	165.6	34.5	564	23	AM684493 NE017F01N
5	165	34.4	548	21	AM329834 N201110E
6	165	34.4	627	24	BE203167 EST403189
7	165	34.4	643	23	AM686778 NF042G08N
8	165	34.4	661	23	BE203464 EST403486
9	165	34.4	671	25	AM980491 EST391644
10	164.6	34.3	540	24	AM755334 S101902.y
11	164.6	34.3	541	18	AV428823 AV428823
12	164	34.2	483	20	BE020246 sm42d08.y
13	163.6	34.1	498	20	AM234941 sf21a03.y
14	163.6	34.1	507	14	AT988606 s03a12.y
15	163.6	34.1	521	24	AM706260 s154b06.y
16	163.6	34.1	521	32	BE020880 sm53e02.y
17	163.6	34.1	522	23	BE022325 sm73d12.y
18	163.6	34.1	537	23	AM568734 s172d11.y
19	163.4	34.0	539	14	AL371451 MtbB44C09
20	163.4	34.0	539	20	AM171714 N100608e
21	163.4	34.0	545	21	AM329829 N201104e
22	163.4	34.0	552	20	AM171725 N100619e
23	163.4	34.0	556	21	AM329581 N200833e
24	163.4	34.0	589	34	BE204913 EST397533
25	163.4	34.0	599	34	BE205354 EST398030
26	163.4	34.0	611	23	AM586090 EST317713
27	163.4	34.0	633	34	AM559608 EST314656
28	163.4	34.0	646	34	BE239885 EST403934
29	163.4	34.0	653	34	BE240619 EST404668
30	163.4	34.0	660	34	BE202706 EST402728
31	163.4	34.0	704	25	AM981477 EST392630
32	162.6	33.9	521	24	AM706169 s152f12.y
33	162.6	33.9	530	32	BE021814 sm62905.y
34	162.6	33.9	660	34	BE320153 NF025F10R
35	162	33.8	481	11	AT495836 sb16h02.y
36	162	33.8	496	23	AM598545 s144h02.y
37	162	33.8	518	32	BE020471 sm44b10.y
38	162	33.8	524	20	AM234671 st17h10.y
39	162	33.8	526	23	AM569426 s187a04.y
40	162	33.8	528	23	BE022155 sm68b09.y
41	162	33.8	528	34	BE210961 s055g08.y
42	161.8	33.7	620	34	BE239825 EST403874
43	161.8	33.7	720	24	AM775813 EST334878
44	161.6	33.7	557	23	AM666076 SK31909.y
45	161.4	33.6	598	23	AM587229 EST318852

ALIGNMENTS

RESULT 1
AM719509

LOCUS	AM719509	551 bp	mRNA	EST	19-APR-2000
DEFINITION	LjNEST5d9r	Lotus japonicus nodule library, mature and immature nodules	Lotus japonicus CDNA 5', mRNA sequence.		
ACCESSION	AM719509				
VERSION	AM719509.1	GI:7614020			
KEYWORDS	EST.				
SOURCE	Lotus japonicus				
ORGANISM	Lotus japonicus				
REFERENCE	1 (bases 1 to 551)				
AUTHORS	Freund, S., Stougaard, J. and Urdavari, M.				
TITLE	Lotus japonicus root nodule ESTs: a tool for functional genomics				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Urdavari MK Molecular Plant Nutrition Max Planck Institute of Molecular Plant Physiology Am Muehlenberg 1, 14476 Golm, Germany Fax: 49 331 567 8250 Email: urdavari@mplm-golm.mpg.de Seq primer: T7 High quality sequence stop: 551. Location/Qualifiers 1..551 /organism="Lotus japonicus" /cultivar="Gifu (B-129)" /db_xref="taxon:34305" /clone_lib="Lotus japonicus nodule library, mature and immature nodules" /note="Organ: Nodule; Vector: pBluescript SK-; Site: 1; EcoRI; Site: 2; XhoI; The library was prepared using mRNA extracted from a mixture of mature (pink) and immature (white) nodules of Lotus japonicus ecotype 'Gifu'. Nodules were induced by, and contained Mesorhizobium loti strain N2P2235."				
BASE COUNT	154 a	129 c	122 g	146 t	
ORIGIN					
Query Match	37.5%;	Score 180;	DB 24;	Length 551;	
Best Local Similarity	62.6%;	Pred. No. 2.5e-42;			
Matches 298; Conservative	0;	Mismatches 175;	Indels 3;	Gaps 1;	
QY	1	ggtgtgttataatagagagagacacactcgtatacccaagcactgacgttcaag	60		
DB	73	GGGTGTTTCACTTCCAGATGAGACTCACTCCACTGTTCCCCAGCTAGGCTTACAA	132		
QY	61	gccttaacctgtagcgagtaaccctcttccaaaggtgacaccacacatgaagcag	120		
DB	133	GCTCTCAACCATAGATGATGATTCATCATCCCAAGGTTCTTCC---AGGTTCAAAAGT	189		
QY	121	gttgaanaacattgaaggaatgaaggccttggaacattagaagaatcagcttccgaa	180		
DB	190	GTTCGAATTTGTTAAAGAAATGCGAGTCCGGAACCATCAAGAAATCACTTTCGAGGAA	249		
QY	181	ggcctcccttcataagtagcgaaggaagcagaggtgtaggagtgagacacacaaact	240		
DB	250	GATGGCAAAACCAAGGACCTGTTGCACAAATTTGAATTCATATGATGAGGCAATTTCCGA	309		
QY	241	tacaattacacgctgtagcagagcggtlcccatagcgacacatgtgagaagaatc	300		
DB	310	TACAGCTACAGCATCATTTGAGGTTCTGACCTTCAGAGACATGAGAGAAATCTATT	369		
QY	301	gagataaagatagtggaacccctgtagtgagagatccatcttggaatcagcaaac	360		
DB	370	GAGGCCAAATTTGGTGGAGGCGCTGATGAGGAGTTCATTGCAACGCTCAGAGTAC	429		
QY	361	cacaccaaagtgtagcagtagtgtagaagcgagagcagtgtaagcagtaagaatgg	420		
DB	430	CACACCAAAAGTAGCGTACCCCTCTGAAGAGAGATATCAAGGCTGGCAGGCGGT	489		
QY	421	gagacacttttgagggcgcttgtagagactactcttgcaacatccgatgctctaca	476		

Db 490 GATGCTTTTCAAGCGGTGAGGGTTACGTTTGGCCACCCGATTACACTA 545

RESULT 2
 AM782077 536 bp mRNA EST 12-MAY-2000
 LOCUS sm01b05.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-c1027-7594 5' similar to TR:P93333 P93333 PR10-1 PROTEIN. [2]
 TR:043350 ; mRNA sequence.

ACCESSION
 AM782077
 VERSION
 AM782077.1 GI:7796683
 KEYWORDS
 EST.
 SOURCE
 soybean.
 ORGANISM
 Glycine max
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 Fabales; Fabaceae; Papilionoideae; Glycine.

REFERENCE
 1 (bases 1 to 536)
 Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Corryell,V., Khanna,
 A., Bolla,B., Marra,M., Haller,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,
 R., Rittler,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,
 R., Materston,R. and Wilson,R.
 Public Soybean EST Project
 Unpublished (1999)
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: Genome Systems, Inc. 4633 World
 Parkway Circle St. Louis, Missouri 63134 For further information
 call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
 427-3324 or contact: clones@genomesystems.com or
 info@genomesystems.com web site: www.genomesystems.com
 High quality sequence stop: 412.
 Location/Qualifiers
 1..536
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1027-7594"
 /clone_lib="Gm-c1027"
 /tissue_type="cotyledons of 3- and 7-day-old Williams
 seedlings"
 /lab_host="DH10B"
 /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
 XhoI; This cDNA library was constructed from mRNA isolated
 from cotyledons of 3- and 7-day-old Williams seedlings
 which were propagated on paper towels with distilled
 water. The cotyledons were flash-frozen in liquid
 nitrogen, then lyophilized for 72 hours. Unequal amounts
 of mRNA was used for cDNA synthesis. Stratagene's cDNA
 Synthesis Kit (catalog number 200401) was used to
 synthesize the cDNA. First-stranded synthesis was
 performed with 5-methyl dCTP, hence the ligated cDNA was
 hemimethylated. A modification of Stratagene's
 first-strand synthesis primer was used. An anchor
 nucleotide (V-A, C, or G) was added to the 3' end of the
 primer (GAGAGAGAGAGAGAGAGACAGTCAG(T)18) to anchor
 the primer at the 5' end of the poly(A) tract. After
 second-strand synthesis, the cDNA ends were filled in
 with cloned pfu DNA, ligated to EcoRI adapters and
 subsequently phosphorylated. The XhoI site within the
 first-strand synthesis primer was then restricted by
 digestion with XhoI; all XhoI sites in the cDNA would be
 protected by their hemimethylated status. The cDNA
 constructs were size-fractionated with a 500 bp cutoff,
 using G130BRL Life Technologies' cDNA Size Fractionation
 column. The column eluent was then ligated into

Stratagene's pBluescript(II) SK+ Predigested vector
 (pBluescript II SK+) that has been digested with EcoRI
 and XhoI, and phosphorylated by Stratagene). 97% of the
 white and blue colonies appear to contain recombinant
 plasmids with cDNA inserts, based on size (n=30). This
 library was constructed by Dr. Paul Keim and Dr. Virginia
 Corryell."

BASE COUNT 150 a 121 c 113 g 151 t 1 others
 ORIGIN

Query Match 35.6%; Score 171; DB 24; Length 536;
 Best Local Similarity 61.8%; Pred. No. 1, le-39;
 Matches 289; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

Qy 1 ggtgtttaatattagatgagaccacacctgttaccacagatcgatcttcaag 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 69 ggtgttttactcagattatgattatgattacccctgctgctctcctttagccttttcmaa 128
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 gcccttacccttgatgagcagatcccttccaaaggttgacaccccaagccaltgacagt 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 129 gccatgacattagatttccatattaccccttccaaagcttctg--ATAGCATCCACAGC 185
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 121 gttgaacattgaaagaaatgagagccttgagaccacaltgaagaagatcgttccgaa 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 186 attgtttttacccacagaaatggtgtcttgcgacacatcagaagatccaccattgaa 245
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 181 ggcctcccttcaagtcagtcagagacagatgtagatgagttgagacacaaacttcaaa 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 246 gctgacaaaacagatattgctgcacacagattgagcattatgagcgttactttgta 305
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 241 tacaattcaagcgttgatcgaagggcggtlcccatagcgcacacattgagaagaatcccaac 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 306 tatatacttgcagcttaactgagggcactgcttgctgcacacattgagagaggtcttatttc 365
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 301 gagataaagatagtcgcaaccccttgatgagatcatcttgaagaatcgcaacaggtac 360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 366 gtagcgcattgtgtgagagctccaaattggagatccattatngagattagttgttcagatt 425
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 361 cacacaaaggtgacacatgagtgagtcagagcagagcttaagaagaagaaatgagtc 420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 426 ttacacaaaagcgatgcttaccgttactgagagagactctaccacaaagccaaagatc 485
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 421 gagacacatttgagggcggttgagagctacaccttggcacacatccgat 468
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 486 caagcgcttgaagacttgaaggggtactgttgaaagcttggcaaatctgatt 533
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
 AM980848
 LOCUS AM980848 698 bp mRNA EST 02-JUN-2000
 DEFINITION EST392001 GVN Medicago truncatula cDNA clone pgVN-58L14, mRNA
 sequence.

ACCESSION
 AM980848
 VERSION
 AM980848.1 GI:8172391
 KEYWORDS
 EST.
 SOURCE
 barrel medic.
 ORGANISM
 Medicago truncatula
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 Fabales; Fabaceae; Papilionoideae; Medicago.

REFERENCE
 1 (bases 1 to 698)
 Fedorova,M., Plesson,B.L., Samac,D.A., Vance,C.P., Gantt,J.S., Peng,
 H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.,
 Holt,I.E. and Fraser,C.M.
 ESTs from one month old nitrogen-fixing root nodules of Medicago
 truncatula
 Unpublished (2000)
 Contact: Carroll P. Vance
 Department of Agronomy and Plant Genetics
 University of Minnesota
 411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
 Tel: 612-625-7219

Fax: 651-649-5058
 Email: vance004@maroon.tc.umn.edu
 University of Minnesota name:M356682e
 TIGR sequence name:MTCB67TK
 More information is available at: <http://chrysie.tamu.edu/medicago>
 Seq primer: Skmod (CTA gaa CTA gta gaa CC).

FEATURES

source
 1..698
 /organism="Medicago truncatula"
 /cultivar="genotype A17"
 /db_xref="taxon:3880"
 /clone="pGVN-58L14"
 /clone_1lb="GVN"
 /tissue_type="N2-fixing root nodules"
 /dev_stage="effective root nodules harvested one month post inoculation with Sinorhizobium meliloti"
 /lab_host="E. coli strain SOLR"
 /note="Vector: pBluescript SK +/-; Site_1: EcoRI, Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meliloti. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Aassist helper phage and propagated in SOLR cells."

BASE COUNT

203 a 108 c 151 g 236 t

ORIGIN

Query Match 34.7%; Score 166.6; DB 25; Length 698;
 Best Local Similarity 60.8%; Pred. No. 2.3e-38;
 Matches 290; Conservative 0; Mismatches 184; Indels 3; Gaps 1;

QY 1 ggtgtgttaataatagagactgagaccactcgttatccagcagctgactggtcaag 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 59 ggtgtgttcaacttgagagactgagaccactcgttatccagcagctgactggtcaag 118
 QY 61 gcccttacccttgagcgatagaccctccttcccaaggctgaccccaagcattagcaat 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 119 gcttttagttacagattctgatatcccttcccaaggctgaccccaagcattagcaat 175
 QY 121 gttgaacacattgaagaaatgagggcctggaacattgaagaagatcagcttccgaa 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 176 attgaattgttgaggaacacgtggcgccggaacatcagaacttacttctgttgaa 235
 QY 181 ggcctcccttcaagtaagtgaggaacagattgtagaggtgagccacaacattcaaa 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 236 ggtgctgaaacaaatgattgattgcaacaaatgagactttagatgattgattgattgct 295
 QY 241 tacaattacagcgatgacgagggcggtcccatagagcagacattgagaagatctcacaac 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 296 tacaactacagcattgattggtggtgacttccagacacatgagagatctctctt 335
 QY 301 gagataaagatagtgcaacccctgtagagagatccatctgaagatcagcaacaagatc 360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 356 gactgtaattgtctgacagggccagatgagatgcatctgcaaaagcttactgtaaatc 415
 QY 361 caccacaaagtgacacagagtgagagcagagtgtaaggaagtaagaataggc 420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 416 ttccacaaagtgatgctgacacacagtgaggaagaaatcagaagtggaagacttagggc 475
 QY 421 gagacactttagagggcggtgagagctaccccttggcagactcgatcctacaac 477
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 476 gatgctcttttcaagcctcttgaaggttgcctttggcacaatcctgattacttaaac 532

RESULT 4
 AM684493 564 bp mRNA EST 15-JUN-2000
 LOCUS
 DEFINITION NF017F01NR1F1000 Nodulated root Medicago truncatula cDNA clone
 ACCESSION
 AM684493

VERSION
 AM684493.1 GI:7559229
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Medicago truncatula
 barrel medic.

REFERENCE

Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
 Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W., May,
 G.D. and Palva,N.L.
 1 (Bases 1 to 564)

TITLE

Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula nodulated root library

JOURNAL

Unpublished (2000)

COMMENT

Contact: Palva NL
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7317
 Fax: 580 221 7380

FEATURES

source
 1..564
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF017F01NR"
 /clone_1lb="Nodulated root"
 /tissue_type="root"
 /dev_stage="Pooled developmental"
 /note="Vector: Lambda zap. Four-week old Rhizobium
 meliloti-inoculated Medicago truncatula roots, containing
 a mixture of young and old roots and nodules."

BASE COUNT

168 a 95 c 125 g 174 t

ORIGIN

Query Match 34.5%; Score 165.6; DB 23; Length 564;
 Best Local Similarity 60.6%; Pred. No. 4.3e-38;
 Matches 289; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

QY 1 ggtgtgttaataatagagactgagaccactcgttatccagcagctgactggtcaag 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 58 ggtgtgttcaacttgagagactgagaccactcgttatccagcagctgactggtcaag 117
 QY 61 gcccttacccttgagcgatagaccctccttcccaaggctgaccccaagcattagcaat 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 118 gcttttagttacagattctgatatcccttcccaaggctgaccccaagcattagcaat 174
 QY 121 gttgaacacattgaagaaatgagggcctggaacattgaagaagatcagcttccgaa 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 175 attgaattgttgaggaacacgtggcgccggaacatcagaacttacttctgttgaa 234
 QY 181 ggcctcccttcaagtaagtgaggaacagattgtagaggtgagccacaacattcaaa 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 235 ggtgctgaaacaaatgattgattgcaacaaatgagactttagatgattgattgattgct 294
 QY 241 tacaattacagcgatgacgagggcggtcccatagagcagacattgagaagatctcacaac 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 295 tacaactacagcattgattggtggtgacttccagacacatgagagatctctctt 354
 QY 301 gagataaagatagtgcaacccctgtagagagatccatctgaagatcagcaacaagatc 360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 355 gactgtaattgtctgacagggccagatgagatgcatctgcaaaagcttactgtaaatc 414
 QY 361 caccacaaagtgacacagagtgagagcagagtgtaaggaagtaagaataggc 420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 415 ttccacaaagtgatgctgacacacagtgaggaagaaatcagaagtggaagacttagggc 474
 QY 421 gagacactttagagggcggtgagagctaccccttggcagactcgatcctacaac 477
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 475 GATGCTTTTCAAGGCTCTTGAANGTTACGTTTGGCAATTCGATTACTAAAGC 531

RESULT 5
AM329834
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AM329834 548 bp mRNA
N201110e rootphos(-) Medicago truncatula cDNA clone MHRP-2AF8, mRNA
sequence.
AM329834
AM329834.2 GI:7676124
EST.
barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
1 (bases 1 to 548)
Harrison,M.J., Liu,J., Harris,A.R., Scott,A.D., Gonzales,R.A.,
Gonzales,M.B. and Ellis,L.
ESTs from phosphate starved roots
Unpublished (1999)
On Jan 28, 2000 this sequence version replaced gi:6800429.
Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5610
Fax: 580-221-7380
Email: mjharrison@noble.org
Date: 1/23/00; Updated to the Database of Expressed Sequence Tags
(dbEST) on 04/27/00; More information is available at
'http://chryslr.tamu.edu/medicago'.
Seq primer: T3.
Location/Qualifiers

FEATURES
source
1..548
/organism="Medicago truncatula"
/cultivar="Jemalong, line A17"
/db_xref="taxon:3880"
/clone_1lb="MHRP-2AF8"
/clone_1lb="rootphos(-)"
/tissue_type="roots"
/dev_stage="phosphate starved"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; At the trifoliolate stage, M. truncatula plants were
transplanted to phosphate-free sand and grown for a
further 30 days. During this 30 day period, they were
fertilized twice weekly with 1/2 Hoaglands solution
containing only 20mM potassium phosphate. RNA was prepared
from the roots. cDNA was prepared from polyA+ enriched
RNA. The cDNA was directionally ligated into the UniZap XR
vector from Stratagene and packaged using Gigapack III
Gold packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-zap phage using
Ex-assist helper phage and propagated in SOLR cells."

BASE COUNT 163 a 92 c 125 g 168 t

ORIGIN

Query Match 34.4%; Score 165; DB 21; Length 548;
Best Local Similarity 60.6%; Pred. No. 6.4e-38;
Matches 289; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

QY 1 ggtgttctaataatgagactgagaccactctgtatccagcagctcgactgttcaag 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 53 GGTGCTTTCAAGCTTTGAGGATGAACCAACATCTATTGACTCTCTAGACTTTACAA 112
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 gcccttacccttgatgcagtaacctcttcacaaaggtgcaccccagaagcactagcagt 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 113 GCTTAACTTACAGATTGTGTAATACCTTATCCCGAAGGTTATTG--ATGCCATCCAAGT 169
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 gtgtgaacaattgagaagaattgagagcctctgtaaccattagaagatcagcttccgaa 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 ATTGAATTTGTGTGAAGAAACGGTGGCGCGAACAACATCAAGAAACTTACTTGTGTA 229
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 ggcctcccttcaagtagctgaaagacagagttgtagtgygaccacacaaccttcaaa 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 230 GGTGCTGAACAAGATGATGATTTGGACAAAGTGACACTAGTATGATGATGATTAACCTT 289
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 tacaattacagcgtgatgtagggcggtcccaataggcgcacatctggagaagaatcccaac 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 290 TTCAACTACACATAGTATGTTGGTGTGTGACTCCAGACACAGTGAGGAAGATCTCCCTTT 349
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 gagataaagatagtgagaccctctgatgagatccatcttgaagatcagcaacaagtagc 360
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 350 GAGTCTAATTTGCTGTGCAGGGCCAGATGAGAGATCATTCGAAACCTTACTGTGAATAC 409
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 cacaccaaggtgacacatgaggtgaaagcagagcaggtlaaggaagtaagaagaaatgggc 420
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 410 TTCAACCAAGGTGATGTCACCTAGTGAAGCAAGTAAGGAGGTAAGGCTAGCGGCT 469
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 gagacacttggagggccgttgtagagactactcttgagacactccgactgactaacac 477
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 GATGCTTTTCAAGGCTCTTGAAGGTTACGTTTGGCAAAATCCTGATTACTAAAGC 526
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
BE203167
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BE203167 627 bp mRNA
EST403189 KVI Medicago truncatula cDNA clone PKV1-4N1, mRNA
sequence.
BE203167
BE203167.1 GI:8746438
EST.
barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
1 (bases 1 to 627)
Vandenbosch,K., Hutt,J., Moore,J., Bergmand,P., Peng,H., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
ESTs from roots of Medicago truncatula after Rhizobium inoculation
Unpublished (1999)
Contact: Vandenbosch K
Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
Email: kate@mail.bio.tamu.edu
Texas A&M University:T262939e
TIGR sequence name:MTAK73TK
More information is available at:
http://chryslr.tamu.edu/medicago
Seq primer: SKmod (CRA gaa gaa ggt gat cc).
Location/Qualifiers

FEATURES
source
1..627
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="PKV1-4N1"
/clone_1lb="KVI"
/tissue_type="Seedling roots"
/dev_stage="24 hours post-inoculation with Sinorhizobium
meliloti ABS7M"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The
cDNA was directionally ligated into the UniZap XR vector
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-zap phage using
Ex-assist helper phage and propagated in SOLR cells."

BASE COUNT 174 a 100 c 147 g 206 t

ORIGIN

Db 341 GAGTCTAAATTCCTGACAGGCGCATGAGATCCATTCGAAGCTTACTGTGAATAC 400
 QY 361 cacaccaaaagtgaccatgagtggaagcagagagtaagcaagtaagaatgagc 420
 Db 401 TTCACCAAGGTATGCTGACCTAGTGAAGAGGAATCAAGGGTGAAGAGCTAGGGGT 460
 QY 421 gagacacttttgaggccgttgagagacactcttcgacacactcgcagtcctaac 477
 Db 461 GATGCTTTTCAAGGCTTGAAGGTTAGCTTTGGCAATCTGATTACTAAGC 517

RESULT 10
 AM755334 540 bp mRNA EST 03-MAY-2000
 LOCUS s101902.X1 GM-cl036 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION GM-cl036-75 5' similar to FR:P93330 P93330 MN13 GENE. ;, mRNA
 sequence.
 ACCESSION AM755334 GI:7684686
 VERSION AM755334
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 Fabales; Fabaceae; Papilionoideae; Glycine.
 1 (bases 1 to 540)
 Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Correll, V., Khanna,
 A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers,
 Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Hallen, N., Schurk,
 R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,
 R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 TITLE Public Soybean EST Project
 JOURNAL Contact: Shoemaker R/Public Soybean EST Project
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available through: Genome Systems, Inc. 4633 World
 Parkway Circle St. Louis, Missouri 63134 For further information
 call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
 427-3334 or contact: clones@genomesystems.com or
 info@genomesystems.com web site: www.genomesystems.com
 High quality sequence stop: 435.
 Location/Qualifiers
 1..540
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: GM-cl036-75"
 /clone_1lb="GM-cl036"
 /rissue_type="somatic embryos cultured on MSD 20"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; site_1: NotI; site_2: SalI; This
 cDNA library was constructed from mRNA isolated from
 somatic embryos (age ranging from 2 months to 9 months)
 cultured on MSD 20. The library was prepared using the
 Life Technologies pSuperScript cDNA library construction
 kit. Complementary DNA was synthesized from mRNA using a
 poly (dT) sequence with a NotI restriction site. SalI
 linkers adapters were ligated to the blunt-ended cDNA
 fragments followed by NotI digestion. The cDNA fragments
 were directionally cloned into the NotI-SalI restriction
 site of the pSPORT1 vector. The ligated cDNA fragments
 were transformed into E.coli Electromax DH10B host cells.
 This library was constructed in the laboratory of Dr. Lila
 Vodkin by Anu Khanna at the University of Illinois at
 Urbana-Champaign. e-mail: l-vodkin@uiuc.edu"

BASE COUNT 167 a 100 c 116 g 156 t 1 others
 ORIGIN

Query Match 34.3%; Score 164.6; DB 24; Length 540;
 Best Local Similarity 60.8%; Pred. No. 8.3e-38;
 Matches 288; Conservative 0; Mismatches 180; Indels 6; Gaps 1;

QY 1 ggtgttctaaltatgagactgagacacactctgttaaccgaagctcagcttcaag 60
 Db 73 GGTGTTTCACTTCTGGAAGGAAACAGCTTCCCGCTCTCTGCGAATAATATACAA 132
 QY 61 gcccttaccttgatgagcagataacctcttccaaaggtgcaccccaagcaltagc 120
 Db 133 GCTATTGCTCTAGATGCGACCAAGTCTTCCCAAAACCATTTGCAATTAAGAGAC 192
 QY 121 gttaaaacattgaggaatgagagccctcggaacacatgaagaatcagcttccgaa 180
 Db 193 GTAGAAACCATTTGAGAGAGATGAGAGGCCAGGAACCTTAAGAACTTACTTGTGAA 252
 QY 181 ggcctcccttcaagtaagtcgtaagagacagatgtgatgagtgagacacacaaactcaaa 240
 Db 253 GG-----TTTAGGTATGTGAAGCACACGCTGATGCAATTCACAGAAACTATGTG 306
 QY 241 tacataacagcgtgatcgagagcggtcccatagggacacatlgagaagatctccaac 300
 Db 307 TACACATATAGTGTGATGGAAGGCGATGTCGAGACCATTTGAGATATGTAT 366
 QY 301 gagataagataagtgagcaacccccctgagagagatccatcttgaagatcagcaacagatc 360
 Db 367 GAGTACCAACTGCTGGCGACACCCAGATGAGAGATCCATTGTGAAGTCCACACCAATATAC 426
 QY 361 cacaccaaaagtgaccatgagtggaagcagagcaagtaagcaagtaagaatggagc 420
 Db 427 TATACCAAGGTATGAGCAACTCGNCGAAATATGTGAAGACTGGAAGAGAGATGC 486
 QY 421 gagacacttttgaggccgttgagagactacctcttgcaacatccagatgcctac 474
 Db 487 GCAGTTTCAACCAAGGCTATTGAGATTTGATTCATTCAGGCTAATCTGATTACAC 540

RESULT 11
 AV428823 541 bp mRNA EST 02-MAY-2000
 LOCUS AV428823 Lotus japonicus young plants (two-week old) Lotus
 DEFINITION japonicus cDNA clone MM073a12_r 5', mRNA sequence.
 ACCESSION AV428823
 VERSION AV428823.1 GI:7678205
 KEYWORDS EST.
 SOURCE Lotus japonicus.
 ORGANISM Lotus japonicus
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 Fabales; Fabaceae; Papilionoideae; Lotus.
 1 (bases 1 to 541)
 Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 Generation of 7137 non-redundant expressed sequence tags from a
 legume, Lotus japonicus
 DNA Res. 7 (2), 127-130 (2000)
 JOURNAL MEDLINE 20277479
 COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp; URL: http://www.kazusa.or.jp/en/plant/
 Location/Qualifiers
 1..541
 /organism="Lotus japonicus"
 /db_xref="taxon:34305"
 /clone="MM073a12_r"
 /clone_1lb="Lotus japonicus young plants (two-week old)"
 /dev_stage="young plants (two-week old)"
 /note="Vector: pBluescriptII SK-; site_1: EcoRI; site_2:
 XhoI; isolate=Miyakojima MG-20"

BASE COUNT 158 a 120 c 113 g 150 t
 ORIGIN

info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 420.

FEATURES

SOURCE

1. .483

/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl028-6568"
/clone_lib="Gm-cl028"
/tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were inoculated with Bradyrhizobium japonicus, strain USDA110 prior to harvest. Stratagene's cDNA synthesis kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dcmp, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A-C, or G) was added to the 3' end of the primer [GAGACGAGACGAGACGAGACTGCAGCTT]18V) to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adaptors and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR predigested vector (pBluescript II SK(+)) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=23). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."

BASE COUNT 157 a 94 c 114 g 118 t

ORIGIN

Query Match 34.2%; Score 164; DB 32; Length 483;
Best Local Similarity 60.8%; Pred. No. 1.2e-37;
Matches 288; Conservative 0; Mismatches 180; Indels 6; Gaps 1;

OY 1 ggctgtttaattatgagaactggagaccacacctgttatccagcagctcgactgtttcaag 60
DB 16 GGTTGTTCACCTTGCGAAGAAGCAACGCTTCCGCCCTGCTGGCGCAAAATTTATACAAA 75

OY 61 gccattacaccttgtagataactctctttccaagtgtgaaccccagaacttagcgt 120
DB 76 GCATTGTGCTAGAGTCCAGCAATGCTCTTCCAAAAAGATTGCCAAATTTATTAAAGAC 135

OY 121 gttaaaacattgaagaaatcgagagsgctggaacattaaagaagaatcatgccttcgaa 180
DB 136 GTAGAACCATTTGAAGAGTAGAGAGGCCAGAGAACATTAAAGAACTTAACCTTCTCTGAA 195

OY 181 ggctcccttcaagtacgtagaagacagagtgtgatgaggtggaaccacaacaatticaa 240
DB 196 GG-----TTTAGGTATTAGTGAAGCACACCAGCTAGTCAATTCAGACACAGAAACTATGTG 249

OY 241 taacaattacacgctgatatgagggggttccattagcgacacattggggaagaattccaac 300
DB 250 TACAACATACTATGCTATTGAAGCGCAGTCCATTGTGCGAGCCATTGGAGAACATATGTTAT 309

OY 301 gagataagaatagtggaacccccctgatatggagatccattctgaagaatcagcaacagrac 360
DB 310 GAGTACAAACTGTGTGGCAACCCAGATGAGAGATTCATTGTGAAAGTCCACAAAGCAAATAC 369

OY 361 cacaccaaaagtgacatgagtgagtgaaagcagagcaggttaaagcgaagttaaagaatggc 420

nucleotide (V-A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI from Promega (400/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using G100BRL Life Technologies' cDNA Size Fractionation column. The column eluent was then precipitated, redissolved, and ligated into Stratagene's Bluescript II XR Predigested vector (pBluescript II SK(+)) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). 100% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=24 and 6, respectively). This library was constructed by Dr. Paul Keim and Dr. Virginia Corvelli.

BASE COUNT 152 a 117 c 124 g 128 t
ORIGIN

Query Match 34.1%; Score 163.6; DB 24; Length 521;
Best Local Similarity 60.5%; Pred. No. 1.6e-37;
Matches 287; Conservative 0; Mismatches 184; Indels 3; Gaps 1;

QY 1 ggtgtgttaattatgagactgagaccactgttatccagagctgactgttcaag 60
DB 51 ggtattttcatttggatgagatgaacaccccttgcctccttaccctttacaaa 110
QY 61 gacctatccttgatgagataacctcttccaaagtlgaccccaagccattagcagt 120
DB 111 gctctagttacagatgccgacaaacgtatccaaaggctgt---gaaagccttcagagagt 167
QY 121 gttgaanaacttgaagaataatgtaggcttgaaccattgaagaatcagcttccgaa 180
DB 168 gttgaaaaccttgagggaacggtggccctggaaacacaaagaaatcatttgccttag 227
QY 181 ggcctcccttcaagtacgtgaagagacagatgtgagtgtagccacaacaacttcaa 240
DB 228 gatggagaaagcaagttgttcttgcacaaatataatcattgacgagcacaacttggga 287
QY 241 tacaattacagcgtgacgagcgtgcctccatagcgacacattgagaagaatcctcaac 300
DB 288 tacagctatagcgttagtgagtggtggcagacacagtcagagaaatcatttcc 347
QY 301 gaagataagatagtgcaacccctgtagtgagatccatttgaagaatcagaacaagtac 360
DB 348 gaatgcgaattgtgctggcgccacgagaggttctgctgggaagctaacgtcaaatatc 407
QY 361 caaccaaaggtagccatgtaggaagcagagcaggttgaagcaagtaagaatgagc 420
DB 408 caaaccaaaagatgctcagccacacacacacacacacacacacacacacacacacac 467
QY 421 gagacactttgagcgcttgagagctacaccttgagacacccgagtcctac 474
DB 468 gatgctcttttcaagccgcttgagagccttaccctttggcgaatcctcatttacaac 521

Search completed: December 11, 2000, 18:36:52
Job time: 29579 sec